RAW SEQUENCE LISTING   DATE: 03/12/2002
PATENT APPLICATION: US/10/084,206   TIME: 14:02:32

Input Set : A:\191D1C1.ST25.txt
Output Set: N:\CRF3\03122002\J084206.raw

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     3 <110> APPLICANT: Li et al.
     5 <120> TITLE OF INVENTION: G-Protein Receptor HTNAD29
     7 <130> FILE REFERENCE: PF191D1C1
C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/084,206
C--> 9 <141> CURRENT FILING DATE: 2002-02-28
     9 <150> PRIOR APPLICATION NUMBER: US95/07288
    10 <151> PRIOR FILING DATE: 1995-06-06
    12 <150> PRIOR APPLICATION NUMBER: 08/468,534
    13 <151> PRIOR FILING DATE: 1995-06-06
    15 <150> PRIOR APPLICATION NUMBER: 09/399,095
    16 <151> PRIOR FILING DATE: 1999-09-20
    18 <160> NUMBER OF SEQ ID NOS: 9
    20 <170> SOFTWARE: PatentIn Version 3.1
    22 <210> SEQ ID NO: 1
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    24 <212> TYPE: DNA
    25 <213> ORGANISM: Homo sapiens
    27 <220> FEATURE:
    28 <221> NAME/KEY: CDS
    29 <222> LOCATION: (523)..(1533)
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    36 catggaagga aaggaatttt aaaaggaaat accaatctct gtgcaaacaa agccttgtat     120
    38 attcatgttt gcaccaatct actgtgagat ttatgaagaa aaacaaattg cggacaactc     180
    40 tctatgtaca cttacaaatg cctcagttga tgcttgtggg ctgtttgtca gcgttctgtg     240
    42 ataatgaaca catggacttc tgtttattaa attcagttga cccctttagc caattgccag     300
    44 gagcctggat ttttacttcc aactgctgat atctgtgtaa aaattgatct acatccaccc     360
    46 tttaaaagca ttgatgaatt aattagaact ttagacaaca agaaaaattg aaaagaattc     420
    48 tcagtaaaag cgaattcgat gttcaaaaca aactacaaag agacaagact tctctgttta     480
    50 ctttctaaga actaatataa ttgctacctt aaaaaggaaa aa atg aac agc aca        534
    51                                               Met Asn Ser Thr
    52                                               1
    54 tgt att gaa gaa cag cat gac ctg gat cac tat ttg ttt ccc att gtt     582
    55 Cys Ile Glu Glu Gln His Asp Leu Asp His Tyr Leu Phe Pro Ile Val
    56 5                   10                  15                  20
    58 tac atc ttt gtg att ata gtc agc att cca gcc aat att gga tct ctg     630
    59 Tyr Ile Phe Val Ile Ile Val Ser Ile Pro Ala Asn Ile Gly Ser Leu
    60                 25                  30                  35
    62 tgt gtg tct ttc ctg caa ccc aag aag gaa agt gaa cta gga att tac     678
    63 Cys Val Ser Phe Leu Gln Pro Lys Lys Glu Ser Glu Leu Gly Ile Tyr
    64             40                  45                  50
    66 ctc ttc agt ttg tca cta tca gat tta ctc tat gca tta act ctc cct     726
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 67 Leu Phe Ser Leu Ser Leu Ser Asp Leu Leu Tyr Ala Leu Thr Leu Pro
 68         55                  60                  65
 70 tta tgg att gat tat act tgg aat aaa gac aac tgg act ttc tct cct       774
 71 Leu Trp Ile Asp Tyr Thr Trp Asn Lys Asp Asn Trp Thr Phe Ser Pro
 72     70                  75                  80
 74 gcc ttg tgc aaa ggg agt gct ttt ctc atg tac atg aag ttt tac agc       822
 75 Ala Leu Cys Lys Gly Ser Ala Phe Leu Met Tyr Met Lys Phe Tyr Ser
 76 85                  90                  95                  100
 78 agc aca gca ttc ctc acc tgc att gcc gtt gat cgg tat ttg gct gtt       870
 79 Ser Thr Ala Phe Leu Thr Cys Ile Ala Val Asp Arg Tyr Leu Ala Val
 80             105                 110                 115
 82 gtc tac cct ttg aag ttt ttt ttc cta agg aca aga aga att gca ctc       918
 83 Val Tyr Pro Leu Lys Phe Phe Phe Leu Arg Thr Arg Arg Ile Ala Leu
 84             120                 125                 130
 86 atg gtc agc ctg tcc atc tgg ata ttg gaa acc atc ttc aat gct gtc       966
 87 Met Val Ser Leu Ser Ile Trp Ile Leu Glu Thr Ile Phe Asn Ala Val
 88         135                 140                 145
 90 atg ttg tgg gaa gat gaa aca gtt gtt gaa tat tgc gat gcc gaa aag      1014
 91 Met Leu Trp Glu Asp Glu Thr Val Val Glu Tyr Cys Asp Ala Glu Lys
 92     150                 155                 160
 94 tct aat ttt act tta tgc tat gac aaa tac cct tta gag aaa tgg caa      1062
 95 Ser Asn Phe Thr Leu Cys Tyr Asp Lys Tyr Pro Leu Glu Lys Trp Gln
 96 165                 170                 175                 180
 98 atc aac ctc aac ttg ttc agg acg tgt aca ggc tat gca ata cct ttg      1110
 99 Ile Asn Leu Asn Leu Phe Arg Thr Cys Thr Gly Tyr Ala Ile Pro Leu
100             185                 190                 195
102 gtc acc atc ctg atc tgt aac cgg aaa gtc tac caa gct gtg cgg cac      1158
103 Val Thr Ile Leu Ile Cys Asn Arg Lys Val Tyr Gln Ala Val Arg His
104             200                 205                 210
106 aat aaa gcc acg gaa aac aag gaa aag aag aga atc ata aaa cta ctt      1206
107 Asn Lys Ala Thr Glu Asn Lys Glu Lys Lys Arg Ile Ile Lys Leu Leu
108         215                 220                 225
110 gtc agc atc aca gtt act ttt gtc tta tgc ttt act ccc ttt cat gtg      1254
111 Val Ser Ile Thr Val Thr Phe Val Leu Cys Phe Thr Pro Phe His Val
112     230                 235                 240
114 atg ttg ctg att cgc tgc att tta gag cat gct gtg aac ttc gaa gac      1302
115 Met Leu Leu Ile Arg Cys Ile Leu Glu His Ala Val Asn Phe Glu Asp
116 245                 250                 255                 260
118 cac agc aat tct ggg aag cga act tac aca atg tat aga atc acg gtt      1350
119 His Ser Asn Ser Gly Lys Arg Thr Tyr Thr Met Tyr Arg Ile Thr Val
120             265                 270                 275
122 gca tta aca agt tta aat tgt gtt gct gat cca att ctg tac tgt ttt      1398
123 Ala Leu Thr Ser Leu Asn Cys Val Ala Asp Pro Ile Leu Tyr Cys Phe
124             280                 285                 290
126 gtt acc gaa aca gga aga tat gat atg tgg aat ata tta aaa ttc tgc      1446
127 Val Thr Glu Thr Gly Arg Tyr Asp Met Trp Asn Ile Leu Lys Phe Cys
128         295                 300                 305
130 act ggg agg tgt aat aca tca caa aga caa aga aaa cgc ata ctt tct      1494
131 Thr Gly Arg Cys Asn Thr Ser Gln Arg Gln Arg Lys Arg Ile Leu Ser
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132      310                     315                     320
134 gtg tct aca aaa gat act atg gaa tta gag gtc ctt gag tagaaccaag      1543
135 Val Ser Thr Lys Asp Thr Met Glu Leu Glu Val Leu Glu
136 325                     330                     335
138 gatgttttga agggaaggga agtttaagtt atgcattatt atatcatcaa gattacattt   1603
140 tgaaaaggaa atctagcatg tgaggggact aagtgttctc agagtgatgt tttaatccag   1663
142 tccaataaaa atatcttaaa actgcattgt acagctccct ccctgcgttt tattaaatga   1723
144 tgtatattaa acaaagatca atattttctt                                   1753
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148 <211> LENGTH: 337
149 <212> TYPE: PRT
150 <213> ORGANISM: Homo sapiens
152 <400> SEQUENCE: 2
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155 1               5                   10                  15
158 Phe Pro Ile Val Tyr Ile Phe Val Ile Val Ser Ile Pro Ala Asn
159             20                  25                  30
162 Ile Gly Ser Leu Cys Val Ser Phe Leu Gln Pro Lys Lys Glu Ser Glu
163         35                  40                  45
166 Leu Gly Ile Tyr Leu Phe Ser Leu Ser Leu Ser Asp Leu Leu Tyr Ala
167     50                  55                  60
170 Leu Thr Leu Pro Leu Trp Ile Asp Tyr Thr Trp Asn Lys Asp Asn Trp
171 65                  70                  75                  80
174 Thr Phe Ser Pro Ala Leu Cys Lys Gly Ser Ala Phe Leu Met Tyr Met
175             85                  90                  95
178 Lys Phe Tyr Ser Ser Thr Ala Phe Leu Thr Cys Ile Ala Val Asp Arg
179         100                 105                 110
182 Tyr Leu Ala Val Val Tyr Pro Leu Lys Phe Phe Phe Leu Arg Thr Arg
183         115                 120                 125
186 Arg Ile Ala Leu Met Val Ser Leu Ser Ile Trp Ile Leu Glu Thr Ile
187     130                 135                 140
190 Phe Asn Ala Val Met Leu Trp Glu Asp Glu Thr Val Val Glu Tyr Cys
191 145             150                 155                 160
194 Asp Ala Glu Lys Ser Asn Phe Thr Leu Cys Tyr Asp Lys Tyr Pro Leu
195             165                 170                 175
198 Glu Lys Trp Gln Ile Asn Leu Asn Leu Phe Arg Thr Cys Thr Gly Tyr
199             180                 185                 190
202 Ala Ile Pro Leu Val Thr Ile Leu Ile Cys Asn Arg Lys Val Tyr Gln
203         195                 200                 205
206 Ala Val Arg His Asn Lys Ala Thr Glu Asn Lys Glu Lys Lys Arg Ile
207     210                 215                 220
210 Ile Lys Leu Leu Val Ser Ile Thr Val Thr Phe Val Leu Cys Phe Thr
211 225             230                 235                 240
214 Pro Phe His Val Met Leu Leu Ile Arg Cys Ile Leu Glu His Ala Val
215             245                 250                 255
218 Asn Phe Glu Asp His Ser Asn Ser Gly Lys Arg Thr Tyr Thr Met Tyr
219             260                 265                 270
222 Arg Ile Thr Val Ala Leu Thr Ser Leu Asn Cys Val Ala Asp Pro Ile
223         275                 280                 285
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226 Leu Tyr Cys Phe Val Thr Glu Thr Gly Arg Tyr Asp Met Trp Asn Ile
227     290             295             300
230 Leu Lys Phe Cys Thr Gly Arg Cys Asn Thr Ser Gln Arg Gln Arg Lys
231 305             310             315             320
234 Arg Ile Leu Ser Val Ser Thr Lys Asp Thr Met Glu Leu Glu Val Leu
235             325             330             335
238 Glu
242 <210> SEQ ID NO: 3
243 <211> LENGTH: 327
244 <212> TYPE: PRT
245 <213> ORGANISM: Homo sapiens
247 <400> SEQUENCE: 3
249 Asp Ser Ser His Met Asp Ser Glu Phe Arg Tyr Thr Leu Phe Pro Ile
250 1             5             10             15
253 Val Tyr Ser Ile Ile Phe Val Leu Gly Val Ile Ala Asn Gly Tyr Val
254             20             25             30
257 Leu Trp Val Phe Ala Arg Leu Tyr Pro Cys Lys Lys Phe Asn Glu Ile
258             35             40             45
261 Lys Ile Phe Met Val Asn Leu Thr Met Ala Asp Met Leu Phe Leu Ile
262     50             55             60
265 Thr Leu Pro Leu Trp Ile Val Tyr Tyr Gln Asn Gln Gly Asn Trp Ile
266 65             70             75             80
269 Leu Pro Lys Phe Leu Cys Asn Val Ala Gly Cys Leu Phe Phe Ile Asn
270             85             90             95
273 Thr Tyr Cys Ser Val Ala Phe Leu Gly Val Ile Thr Tyr Asn Arg Phe
274             100             105             110
277 Gln Ala Val Thr Arg Pro Ile Lys Thr Ala Gln Ala Asn Thr Arg Lys
278             115             120             125
281 Arg Gly Ile Ser Leu Ser Leu Val Ile Trp Val Ala Ile Val Gly Ala
282     130             135             140
285 Ala Ser Tyr Phe Leu Ile Leu Asp Ser Thr Asn Thr Val Pro Asp Ser
286 145             150             155             160
289 Ala Gly Ser Gly Asn Val Thr Arg Cys Phe Glu His Tyr Glu Lys Gly
290             165             170             175
293 Ser Val Pro Val Leu Ile Ile His Ile Phe Ile Val Phe Ser Phe Phe
294             180             185             190
297 Leu Val Phe Leu Ile Ile Leu Phe Cys Asn Leu Val Ile Ile Arg Thr
298             195             200             205
301 Leu Leu Met Gln Pro Val Gln Gln Gln Arg Asn Ala Glu Val Thr Gly
302     210             215             220
305 Arg Ala Leu Trp Met Val Cys Thr Val Leu Ala Val Phe Ile Ile Cys
306 225             230             235             240
309 Phe Val Pro His His Val Val Gln Leu Pro Trp Thr Leu Ala Glu Leu
310             245             250             255
313 Gly Phe Gln Asp Ser Lys Phe His Gln Ala Ile Asn Asp Ala His Gln
314             260             265             270
317 Val Thr Leu Cys Leu Leu Ser Thr Asn Cys Val Leu Asp Pro Val Ile
318             275             280             285
321 Tyr Cys Phe Leu Thr Lys Lys Phe Arg Lys His Leu Thr Glu Lys Phe
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322   290   295   300
325 Tyr Ser Met Arg Ser Ser Arg Lys Cys Ser Arg Ala Thr Thr Asp Thr
326 305   310   315   320
329 Val Thr Glu Val Val Val Pro
330   325
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334 <211> LENGTH: 29
335 <212> TYPE: DNA
336 <213> ORGANISM: Artificial sequence
338 <220> FEATURE:
339 <223> OTHER INFORMATION: Contains an EcoRI restriction enzyme site
341 <400> SEQUENCE: 4
342 cgaattcctc catgaacagc acatgtatt   29
345 <210> SEQ ID NO: 5
346 <211> LENGTH: 29
347 <212> TYPE: DNA
348 <213> ORGANISM: Artificial sequence
350 <220> FEATURE:
351 <223> OTHER INFORMATION: Contains complementary sequences to a HindIII site
353 <400> SEQUENCE: 5
354 cggaagcttc gtcaaggacc tctaattcc   29
357 <210> SEQ ID NO: 6
358 <211> LENGTH: 34
359 <212> TYPE: DNA
360 <213> ORGANISM: Artificial sequence
362 <220> FEATURE:
363 <223> OTHER INFORMATION: Contains a HindIII site
365 <400> SEQUENCE: 6
366 gtccaagctt gccaccatga acagcacatg tatt   34
369 <210> SEQ ID NO: 7
370 <211> LENGTH: 61
371 <212> TYPE: DNA
372 <213> ORGANISM: Artificial sequence
374 <220> FEATURE:
375 <223> OTHER INFORMATION: Contains complementary sequences to an XhoI site,
376   translation stop codon, and an HA tag
378 <400> SEQUENCE: 7
379 ctagctcgag tcaagcgtag tctgggacgt cgtatgggta gcaaggacct ctaattccat   60
381 a   61
384 <210> SEQ ID NO: 8
385 <211> LENGTH: 30
386 <212> TYPE: DNA
387 <213> ORGANISM: Artificial sequence
389 <220> FEATURE:
390 <223> OTHER INFORMATION: Contains a BamHI restriction enzyme site followed by 4
nucleotides resembling an efficient signal for the initiation
391   of translation in eukaryotic cells
393 <400> SEQUENCE: 8
394 cgggatccct ccatgaacag cacatgtatt   30
397 <210> SEQ ID NO: 9

Input Set : A:\191D1C1.ST25.txt
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L:9 M:270 C: Current Application Number differs, Replaced Current Application No
L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date